

## 10086816 Results

SEQ ID NO: 2

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2849	100.0	550	21	AA44278	Human organic anio
2	2849	100.0	550	22	AAB47271	hOAT1. Homo sapie
3	2832.5	99.4	563	20	AAW88489	Human organic anio
4	2538.5	89.1	551	20	AAW88488	Rat organic anion
5	2463.5	86.5	545	22	AAB36553	Mouse organic anio
6	1416	49.7	542	22	AAB47274	hOAT3. Homo sapie
7	1415	49.7	542	21	AA492902	Human cerebral org
8	1373.5	48.2	561	18	AAW44196	Human osteoclast t
9	1371	48.1	537	18	AAW44195	Mouse osteoclast t
10	1370	48.1	536	21	AA492903	Rat cerebral organ
11	1287.5	45.2	557	24	ABU54646	Human NOVX polypep
12	1266.5	44.5	556	24	ABJ37918	NOVX protein seque
13	1264	44.4	584	23	ABP70090	Human NOV18a. Hom
14	1250	43.9	589	23	AAE13280	Human transporters
15	1249.5	43.9	573	24	ABJ37917	NOVX protein seque
16	1231	43.2	778	24	ABP54440	Human TCH110 prote
17	1227.5	43.1	553	22	AAE10332	Human transporter
18	1227.5	43.1	553	23	ABP70091	Human NOV19a. Hom
19	1211.5	42.5	815	22	ABG26899	Novel human diagno
20	1208	42.4	578	22	AAE06571	Human protein havi
21	1173.5	41.2	553	24	ABG73329	Human organic ion
22	1133	39.8	550	22	AAE06612	Human protein havi
23	1133	39.8	550	22	AAB69091	Human organic anio
24	1133	39.8	550	23	AAE16772	Human transporter
25	1133	39.8	550	24	ABB82969	Human SLC22A relat

## RESULT 1

AA44278

ID AA44278 standard; Protein; 550 AA.

XX

AC AA44278;

XX

DT 29-FEB-2000 (first entry)

XX

DE Human organic anion transporter.

XX

KW Human organic anion transporter; hOAT; nephrotoxic compound; screen;  
KW drug-drug interaction; nucleotide phosphonate.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 515..528

FT /label= Immunogen

FT /note= "For producing antibodies"

XX

PN W09964459-A2.

XX

PD 16-DEC-1999.

XX

PF 10-JUN-1999; 99WO-US13172.

XX

PR 11-JUN-1998; 98US-0088864.

PR 03-MAY-1999; 99US-0132267.

XX

PA (GILE-) GILEAD SCI INC.

XX

PI Cihlar T;

XX

DR WPI; 2000-097519/08.

XX

RT

XX

111  
DC

XX

CC

XX

1

Db

1

Qy

Db

Qy

Db

Qy

•

Db

AAB47271

XX

AC

DT 06-AUG-2001 (first entry)  
 XX  
 DE hOAT1.  
 XX  
 KW Human; organic anion transporter; hOAT; liver; kidney;  
 KW membrane protein; transport; organic anion; splice variant.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 271  
 FT /note= "PKC phosphorylation site"  
 FT Modified-site 278  
 FT /note= "PKC phosphorylation site"  
 FT Modified-site 284  
 FT /note= "PKC phosphorylation site"  
 XX  
 PN WO200104283-A2.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 12-JUL-2000; 2000WO-US18980.  
 XX  
 PR 12-JUL-1999; 99US-0143771.  
 XX  
 PA (META-) METABASIS THERAPEUTICS INC.  
 XX  
 PI Sun W;  
 XX  
 DR WPI; 2001-367057/38.  
 DR N-PSDB; AAC85819.  
 XX  
 PT Nucleic acids encoding human organic anion transporter polypeptides,  
 PT useful in gene therapy procedures -  
 XX  
 PS Example 2; Fig 1; 95pp; English.  
 XX  
 CC The sequences given in AAB47271-76 represent human organic anion  
 CC transporter (hOAT) polypeptides. hOAT polypeptides are preferentially  
 CC expressed in the liver and kidneys of humans. OAT's are membrane  
 CC proteins that facilitate the transport of organic anions across the  
 CC cell membrane. The mechanism of transport is thought to be a secondary  
 CC or tertiary active transport involving exchange of another organic anion.  
 CC hOAT2A and hOAT2B are thought to be splice variants as they are  
 CC identical except at the C-terminal end. hOAT proteins and the DNA  
 CC encoding them, may be used in the prevention, treatment and diagnosis  
 CC of diseases associated with inappropriate hOAT expression.  
 XX  
 SQ Sequence 550 AA;  
  
 Query Match 100.0%; Score 2849; DB 22; Length 550;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-281;  
 Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 MAFNDLLQQVGGVGRFQQIQVTLVVLP LLLMASHNTLQNFTAAIPTHHCRPPADANLSKN 60  
 |||  
 Db 1 MAFNDLLQQVGGVGRFQQIQVTLVVLP LLLMASHNTLQNFTAAIPTHHCRPPADANLSKN 60  
  
 QY 61 GGLEVWLPDRDQGQPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI 120  
 |||  
 Db 61 GGLEVWLPDRDQGQPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI 120  
  
 QY 121 VTEWDLVCSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLILNYLQTAVSGTCAA 180  
 |||  
 Db 121 VTEWDLVCSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLILNYLQTAVSGTCAA 180  
  
 QY 181 FAPNFPPIYCAFRLLSGMALAGISLNCMTLNVEWMPHTRACVGTIGYVYSLGQFLLAGV 240  
 |||  
 Db 181 FAPNFPPIYCAFRLLSGMALAGISLNCMTLNVEWMPHTRACVGTIGYVYSLGQFLLAGV 240  
  
 QY 241 AYAVPHWRHLQLLVSAFFFAFFIYSWFFIESARWHSSSGRDLTLRALQRVARINGKREE 300

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Db      241  |||||AYAVPHWRHLQLLVSAFFFAFFIYSWFFIESARWHSSSGRLDLTLRALQRVARINGKREE 300
QY      301  GAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHLFLCLSMWLFATSFAYYGLVMDL 360
Db      301  |||||GAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHLFLCLSMWLFATSFAYYGLVMDL 360
QY      361  QGFGVSIYLIQVIFGAVDLPKLVGFLVINSIGRRPAQMAALLLAGICILLNGVIPQDQS 420
Db      361  |||||QGFGVSIYLIQVIFGAVDLPKLVGFLVINSIGRRPAQMAALLLAGICILLNGVIPQDQS 420
QY      421  IVRTSLAVLGKGLAASFNCIFLYTGELYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE 480
Db      421  |||||IVRTSLAVLGKGLAASFNCIFLYTGELYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE 480
QY      481  LYPSMPLFIYGAVPVAASAVTVLLPETLGQPLPDTVDLESRKKGQTRQQQEHQKYMVPL 540
Db      481  |||||LYPSMPLFIYGAVPVAASAVTVLLPETLGQPLPDTVDLESRKKGQTRQQQEHQKYMVPL 540
QY      541  QASAEKKNGL 550
Db      541  |||||QASAEKKNGL 550

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RESULT 3

AAW88489

ID AAW88489 standard; Protein; 563 AA.

XX

AC AAW88489;

XX

DT 05-MAR-1999 (first entry)

XX

DE Human organic anion transporter OAT-1.

XX

KW Organic anion transporter; OAT-1; nephrotoxicity; drug release;  
 KW drug-drug interaction mechanism; drug elimination; kidney;  
 KW beta-lactam antibiotic; non-steroidal antiinflammatory; diuretic.

XX

OS Homo sapiens.

XX

PN WO9853064-A1.

XX

PD 26-NOV-1998.

XX

PF 18-MAY-1998; 98WO-JP02171.

XX

PR 23-MAY-1997; 97JP-0134182.

XX

PA (TANA) TANABE SEIYAKU CO.

XX

PI Endou H, Hosoyamada M, Kanai Y, Sekine T;

XX

DR WPI; 1999-045310/04.

DR N-PSDB; AAV79585.

XX

PT New renal organic anion transporter protein - useful for, e.g.  
 PT screening potential drugs for prevention of nephrotoxicity and as a  
 PT reagent for the investigation of drug metabolism

XX

PS Claim 1; Page 27-32; 45pp; Japanese.

XX

CC The present sequence represents human organic anion transporter protein  
 CC OAT-1. OAT-1 may be used as a reagent for the in vitro analysis and  
 CC study of drug release and drug-drug interaction mechanisms and drug  
 CC elimination via the kidney (e.g. for drugs such as beta-lactam  
 CC antibiotics, non-steroidal antiinflammatories and diuretics), and as  
 CC a reagent for screening candidate drugs for the prevention of  
 CC nephrotoxicity. Oligonucleotide sequences which hybridise to the OAT-1  
 CC polynucleotide may be used as probes for detection of OAT-1 gene  
 CC sequences.

SQ Sequence 563 AA;

Qy	1	MAFNDDLQQQVGVGGRFQQIQVTLVVLP LLLMASHNTLQNFTAAIPTHHCRPPADANLSKN	60
Db	1	MAFNDDLQQQVGVGGRFQQIQVTLVVLP LLLMASHNTLQNFTAAIPTHHCRPPADANLSKN	60
Qy	61	GGLEVWLPDRDQQQPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGIYDNTSFPSTI	120
Db	61	GGLEVWLPDRDQQQPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGIYDNTSFPSTI	120
Qy	121	VTEWDLVCSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLILNYLQTAVSGTCAA	180
Db	121	VTEWDLVCSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLILNYLQTAVSGTCAA	180
Qy	181	FAPNFPIYCAFRLLSGMALAGISLNCMTLNVEWMPIHTRACVGTIGYVYSLGQFLLAGV	240
Db	181	FAPNFPIYCAFRLLSGMALAGISLNCMTLNVEWMPIHTRACVGTIGYVYSLGQFLLAGV	240
Qy	241	AYAVPHWRHLQLLVSAFFFAFFIYSWFFIESARWHSSSGRLDLTLRALQRVARINGKREE	300
Db	241	AYAVPHWRHLQLLVSAFFFAFFIYSWFFIESARWHSSSGRLDLTLRALQRVARINGKREE	300
Qy	301	GAKLSMEVLRASLQKELTMGKGQASAMELLRCPTRLRHLFLCLSMLWFATSFAYYGLVMDL	360
Db	301	GAKLSMEVLRASLQKELTMGKGQASAMELLRCPTRLRHLFLCLSMLWFATSFAYYGLVMDL	360
Qy	361	QGFGVSIYLIQVIFGAVDLPALVGLVINSLGRRPAQMAALLLAGICILLNGVIPQDQS	420
Db	361	QGFGVSIYLIQVIFGAVDLPALVGLVINSLGRRPAQMAALLLAGICILLNGVIPQDQS	420
Qy	421	IVRTSLAVLGKGCLAASFNCIFLYTGELYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE	480
Db	421	IVRTSLAVLGKGCLAASFNCIFLYTGELYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE	480
Qy	481	LYPSMPLFIYGAVPVAASAVTVLLPETLGQPLPDTVQDLES-----RKGKQT	527
Db	481	LYPSMPLFIYGAVPVAASAVTVLLPETLGQPLPDTVQDLESRWAPTQKEAGIYPRKGKQT	540
Qy	528	RQQQEHQKYMVPLQASAEKNGL	550
Db	541	RQQQEHQKYMVPLQASAEKNGL	563

Issued:

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2849	100.0	550	4	US-09-330-245A-2	Sequence 2, Appli
2	2463.5	86.5	545	4	US-09-572-147-2	Sequence 2, Appli
3	1371	48.1	537	2	US-08-647-397-2	Sequence 2, Appli
4	704	24.7	556	3	US-08-501-572-1	Sequence 1, Appli
5	704	24.7	556	3	US-09-040-444-1	Sequence 1, Appli
6	699.5	24.6	555	3	US-08-501-572-3	Sequence 3, Appli
7	699.5	24.6	555	3	US-09-040-444-3	Sequence 3, Appli
8	674	23.7	553	3	US-08-501-572-2	Sequence 2, Appli
9	674	23.7	553	3	US-09-040-444-2	Sequence 2, Appli

RESULT 2  
US-09-572-147-2  
; Sequence 2, Application US/09572147

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; Patent No. 6420544
; GENERAL INFORMATION:
; APPLICANT: Lin Yue
; APPLICANT: John Feild
; APPLICANT: Harma Ellens
; TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: ENCODING MURINE ORGANIC ANION TRANSPORTER 5 (mOATP5) AND
; TITLE OF INVENTION: SCREENING METHODS THEREOF
; FILE REFERENCE: GP-70622
; CURRENT APPLICATION NUMBER: US/09/572,147
; CURRENT FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 60/134,879
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 545
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
US-09-572-147-2

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Query Match      86.5%; Score 2463.5; DB 4; Length 545;
Best Local Similarity 85.1%; Pred. No. 8.9e-251;
Matches 469; Conservative 41; Mismatches 34; Indels 7; Gaps 2;

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Qy      1 MAFNDLLQQVGGVGRFQQIQVTLVVLPLLLMASHNTLQNFTAAIPTHHCRPPADANLSKN 60
      |||:|||||:|||||:| |||||:|||||:|||||:|||||:|||||:
Db      1 MAFNDLLKQVGGVGRFQLIQVTMVVAPLLLMAHNTLQNFTAAIPAHHCRPPANANLSKD 60

Qy      61 GGLEVWLPRDRQQPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI 120
      ||| ||| |||:||||| | ||||| ||||| ||| |||:|||||
Db      61 GGLEAWLPLDKQGRPESCLRFPFPH-----NGTEANGTGVTEPCLDGWVYDNSTFPSTI 114

Qy      121 VTEWDLVCSHRALRQLAQSLYVMGVLLGAMVFGYLADRLGRRKVLILNYLQTAVSGTCAA 180
      |||:||||| |||||:|||||:|||||:|||||:|||||:|||||
Db      115 VTEWNLVCSHRAFRQLAQSLFMVGVLLGAMMFGYLADRLGRRKVLILNYLQTAVSGTCAA 174

Qy      181 FAPNFPIYCAFRLLSGMLAGISLNCMTLNVEMMPIHTRACVGTILIGYVYSLGQFLLAGV 240
      :||: :| |||||:| ||:|||||:|||||:|||||:|||||:
Db      175 YAPNYTVYICFRLLSGMSLASIAINCMTLNMEWMPIHTRAYVGTILIGYVYSLGQFLLAGI 234

Qy      241 AYAVPHWRHLQLLVSAPFFAFFIYSWFFIESARWHSSSGRLDLTLRALQVRVINGKREE 300
      |||||:||||| || ||| |||||:|||||:|||||:|||||:|||||
Db      235 AYAVPHWRHLQLAVSVPPFFVAFIYSWFFIESARWYSSSGRLDLTLRALQVRVINGKQEE 294

Qy      301 GAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHLFLCLSMLWFATSFAYYGLVMDL 360
      ||||:|||: |||||: |||||:|||||:|||||:|||||:|||||
Db      295 GAKLSIEVLQTSLQKELTLNKGQASAMELLRCPTLRRLFLCLSMLWFATSFAYYGLVMDL 354

Qy      361 QGFGVSIYLIQVIFGAVDLPKLVGLVINSLGRRPAQMAALLLAGICILLNGVIPQDQS 420
      ||||:|||||:||||| || ||||:|||||:|||||:|||||:|||||:
Db      355 QGFGVSMYLIQVIFGAVDLPKLVGLVINSMGRRPAQLASLLLAGICILVNGIIPRGHT 414

Qy      421 IVRTSLAVLGKGCLAASFNCIFLYTGELYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE 480
      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      415 IIRTS LAVLGKGCLASSFNCIFLYTGELYPTMIRQTGLGMGSTMARVGSIVSPLISMTAE 474

Qy      481 LYPSMPLFIYGAVPVAASAVTVLLPETLGQPLPDTVQDLESR-KGKQTRQQEHQKYMVP 539
      |||:||||:||||| |||||:|||||:|||||:||||:||||:|
Db      475 FYPSIPLFIFGAVPVAASAVTALLPETLGQPLPDTVQDLKSRSRGKQKQQLEQQKQMIP 534

Qy      540 LQASAEKKNGL 550
      || |||||
Db      535 LQVSTQEKKNGL 545

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#### SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	723	25.4	593	2	JC4884	organic cation tra
2	709	24.9	556	2	S50862	organic cation tra
3	644.5	22.6	576	2	T22509	hypothetical prote
4	641	22.5	557	2	JW0089	organic cation tra
5	617.5	21.7	557	2	JE0346	high-affinity carn
6	450.5	15.8	794	2	T27870	hypothetical prote
7	450	15.8	745	2	T16565	hypothetical prote
8	434.5	15.3	539	2	C96758	probablle protein
9	408.5	14.3	515	2	B96825	hypothetical prote
10	401.5	14.1	527	2	T01019	transport protein
11	395.5	13.9	447	2	D89646	protein ZK455.8 [i
12	391	13.7	521	2	H86298	hypothetical prote

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	734.5	25.8	556	1	OCN3_HUMAN	O75751 homo sapien
2	696.5	24.4	551	1	OCN3_MOUSE	Q9wtw5 mus musculu
3	696.5	24.4	551	1	OCN3_RAT	O88446 rattus norv
4	641	22.5	557	1	OCN2_HUMAN	O76082 homo sapien
5	639.5	22.4	557	1	OCN2_MOUSE	Q9z0e8 mus musculu
6	630.5	22.1	557	1	OCN2_RAT	O70594 rattus norv
7	400.5	14.1	464	1	YT13_CAEEL	Q10917 caenorhabdi
8	387	13.6	529	1	YOU1_CAEEL	P30638 caenorhabdi
9	352.5	12.4	516	1	BOCT_RAT	Q9p290 rattus norv

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2849	100.0	550	4	Q8N192	Q8n192 homo sapien
2	2832.5	99.4	563	4	O95742	O95742 homo sapien
3	2600	91.3	506	4	Q9NQC2	Q9nqc2 homo sapien
4	2583.5	90.7	519	4	Q9NQA6	Q9nqa6 homo sapien
5	2571.5	90.3	551	6	Q9TSY7	Q9tsy7 oryctolagus
6	2549.5	89.5	551	11	O35956	O35956 rattus norv
7	2524.5	88.6	547	6	Q8MK48	Q8mk48 sus scrofa
8	2463.5	86.5	545	11	Q8VC69	Q8vc69 mus musculu
9	2449.5	86.0	545	11	Q61185	Q61185 mus musculu
10	2437.5	85.6	533	6	Q8MK47	Q8mk47 sus scrofa
11	1421	49.9	542	6	Q8HY24	Q8hy24 oryctolagus
12	1416	49.7	542	4	Q8TCC7	Q8tcc7 homo sapien

#### RESULT 2

O95742

ID O95742 PRELIMINARY; PRT; 563 AA.

AC O95742; O95187; Q9UEQ8; Q9UBG6;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Renal organic anion transport protein 1.

GN SLC22A6 OR OAT1 OR ROAT1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND CHARACTERIZATION.

RC TISSUE=KIDNEY;

RX MEDLINE=99103997; PubMed=9887087;

RA Hosoyamada M., Sekine T., Kanai Y., Endou H.;

RT "Molecular cloning and functional expression of a multispecific

RT organic anion transporter from human kidney.";

RL Am. J. Physiol. 276:F122-F128(1999).

RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=98433806; PubMed=9762842;  
 RA Reid G., Wolff N.A., Dautzenberg F.M., Burckhardt G.;  
 RT "Cloning of a human renal p-aminohippurate transporter, hROAT1.";  
 RL Kidney Blood Press. Res. 21:233-237(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY;  
 RX MEDLINE=99137667; PubMed=9950961;  
 RA Lu R., Chan B.S., Schuster V.L.;  
 RT "Cloning of the human kidney PAH transporter: narrow substrate  
 RT specificity and regulation by protein kinase C.";  
 RL Am. J. Physiol. 276:F295-F303(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY;  
 RX MEDLINE=99160894; PubMed=10049739;  
 RA Race J.E., Grassl S.M., Williams W.J., Holtzman E.J.;  
 RT "Molecular cloning and characterization of two novel human renal  
 RT organic anion transporters (hOAT1 and hOAT3).";  
 RL Biochem. Biophys. Res. Commun. 255:508-514(1999).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY;  
 RX MEDLINE=99393620; PubMed=10462545;  
 RA Cihlar T., Lin D.C., Pritchard J.B., Fuller M.D., Mendel D.B.,  
 RA Sweet D.H.;  
 RT "The antiviral nucleotide analogs cidofovir and adefovir are novel  
 RT substrates for human and rat renal organic anion transporter 1.";  
 RL Mol. Pharmacol. 56:570-580(1999)..  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Bahn A., Prawitt D., Reid G., Enklaar T., Wolff N.A., Hillemann A.,  
 RA Godehardt S., Buttler D., Knabe M., Schulten H.J., Gunawan B.,  
 RA Fuezesi L., Zabel B., Burckhardt G.;  
 RT "Genomic cloning and characterization of the human renal organic anion  
 RT transporter gene (hOAT1).";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: MEDIATES THE NA(+)-INDEPENDENT TRANSPORT OF ORGANIC  
 CC ANIONS SUCH AS P-AMINOHIPPURATE AND ALPHA-KETOGLUTARATE.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. BASOLATERAL  
 CC MEMBRANE (POTENTIAL).  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HOAT1-1 (SHOWN HERE) AND HOAT1-  
 CC 2; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN KIDNEY. ALSO DETECTED IN  
 CC BRAIN AND AT LOW LEVELS, IN SKELETAL MUSCLE AND PLACENTA. NOT  
 CC EXPRESSED IN HEART, LUNG, LIVER, PANCREAS, COLON, THYMUS, SMALL  
 CC INTESTINE OR PERIPHERAL BLOOD LEUKOCYTES. IN THE KIDNEY, STRONGLY  
 CC EXPRESSED IN PROXIMAL TUBULE CELLS.  
 CC -1- PTM: GLYCOSYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE SLC22 FAMILY OF TRANSPORTERS.  
 DR EMBL; AF057039; AAC70004.1; -.  
 DR EMBL; AB009697; BAA75072.1; -.  
 DR EMBL; AF104038; AAD10052.1; -.  
 DR EMBL; AB009698; BAA75073.1; -.  
 DR EMBL; AF097490; AAD19356.1; -.  
 DR EMBL; AF124373; AAD55356.1; -.  
 DR EMBL; AJ249369; CAB77184.1; -.  
 DR Genew; HGNC:10970; SLC22A6.  
 DR InterPro; IPR007114; MFS.  
 DR InterPro; IPR004749; Orgcat\_transp.  
 DR InterPro; IPR005828; Sub\_transporter.  
 DR Pfam; PF00083; sugar\_tr; 1.  
 DR TIGRFAMs; TIGR00898; 2A0119; 1.  
 DR PROSITE; PS50850; MFS; 1.  
 KW Transmembrane; Transport; Alternative splicing; Ion transport;  
 KW Glycoprotein.  
 FT TRANSMEM 136 156 POTENTIAL.  
 FT TRANSMEM 185 205 POTENTIAL.  
 FT TRANSMEM 249 269 POTENTIAL.  
 FT TRANSMEM 338 358 POTENTIAL.



FT	TRANSMEM	396	416	POTENTIAL.
FT	TRANSMEM	426	446	POTENTIAL.
FT	TRANSMEM	485	505	POTENTIAL.
FT	CARBOHYD	39	39	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	56	56	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	92	92	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	97	97	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	113	113	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPIC	523	535	MISSING (IN ISOFORM HOAT1-2).
FT	CONFLICT	14	14	G -> S (IN REF. 3).
FT	CONFLICT	563	563	L -> F (IN REF. 2).
SQ	SEQUENCE	563 AA;	61816 MW;	74AD3EA2678032E4 CRC64;

Query Match 99.4%; Score 2832.5; DB 4; Length 563;  
 Best Local Similarity 97.7%; Pred. No. 4.4e-227;  
 Matches 550; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy	1	MAFNDDLQQVGGVGRFQQIQVTLVVLPLLLMASHNTLQNFTAAIPTHHCRPPADANLSKN	60
Db	1	MAFNDDLQQVGGVGRFQQIQVTLVVLPLLLMASHNTLQNFTAAIPTHHCRPPADANLSKN	60
Qy	61	GGLEVWLPRDRQQPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGIYDNTSTFPSTI	120
Db	61	GGLEVWLPRDRQQPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGIYDNTSTFPSTI	120
Qy	121	VTEWDLVCSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRKRVLIILNYLQTAVSGTCAA	180
Db	121	VTEWDLVCSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRKRVLIILNYLQTAVSGTCAA	180
Qy	181	FAPNFPFIYCAFRLLSGMALAGISLNCMTLNVEWMPHTRACVGTIGYVYSLGQFLLAGV	240
Db	181	FAPNFPFIYCAFRLLSGMALAGISLNCMTLNVEWMPHTRACVGTIGYVYSLGQFLLAGV	240
Qy	241	AYAVPHWRHLQLLVSAPFFAFFIYSWFFIESARWHSSSGRLDLTLRALQVRVARINGKREE	300
Db	241	AYAVPHWRHLQLLVSAPFFAFFIYSWFFIESARWHSSSGRLDLTLRALQVRVARINGKREE	300
Qy	301	GAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHLFLCLSMWLFATSFAYYGLVMDL	360
Db	301	GAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHLFLCLSMWLFATSFAYYGLVMDL	360
Qy	361	QGFGVSIYLIQVIFGAVDLPKLVGFLVINSIGRRPAQMAALLLAGICILLNGVIPQDQS	420
Db	361	QGFGVSIYLIQVIFGAVDLPKLVGFLVINSIGRRPAQMAALLLAGICILLNGVIPQDQS	420
Qy	421	IVRTSLAVLGKGCLAASFNCIFLYTGELYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE	480
Db	421	IVRTSLAVLGKGCLAASFNCIFLYTGELYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE	480
Qy	481	LYPSMPLFIYGAVPVAASAVTVLLPETLGQPLPDTVQDLES-----RKGKQT	527
Db	481	LYPSMPLFIYGAVPVAASAVTVLLPETLGQPLPDTVQDLESRWAPTQKEAGIYPRKGKQT	540
Qy	528	RQQQEHQKYMVPLQASAEKNGL	550
Db	541	RQQQEHQKYMVPLQASAEKNGL	563

RESULT 6  
035956

ID 035956 PRELIMINARY; PRT; 551 AA.  
 AC 035956;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Renal organic anion transport protein 1.  
 GN SLC22A6 OR ROAT1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



Qy	241	AYAVPWHRHLQLLVSAFFFAFFIYSWFFIESARWHSSSGLDLTLRALQRVARINGKREE	300
		:           :           :           :           :	
Db	241	AYAVPWHRHLQLVSVFPFIIAFIYSWFFIESARWYSSSGLDLTLRALQRVARINGKQEE	300
Qy	301	GAKLSMEVLRLASLQKELTMGKGQASAMELLRCPTLRHFLCLSMWFATSFAYYGLVMDL	360
		:         :	
Db	301	GAKLSIEVLRSLQKELTSLSGKQASAMELLRCPTLRHFLCLSMWFATSFAYYGLVMDL	360
Qy	361	QGFGVSIYLIQVIFGAVDLPALGVGFLVINSLGRRPQAAMALLLAGICILNGVIPDQS	420
		:                             :         :         :   :   : :	
Db	361	QGFGVSMYLIQVIFGAVDLPKFVCFLVINSMGRRPAQMASLLLLAGICILVNGIIPKSHT	420
Qy	421	IVRTSLAVLGKGCLAASFNCIFLYTGELYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE	480
		:           :           :           :           :           :	
Db	421	IIRTSLAVLGKGCLASSFNCIFLYTGELYPTVIRQTGLMGSTMARVGSIVSPLVSMTAE	480
Qy	481	LYPSPMLFIYGAVPVAAASAVTVLLPETLGQPLPDTVQDLESR-KGKTTRQQQEHHQKMVP	539
		:         :         :         :         :         :	
Db	481	FYPSPMLFIFGAVPVVASAVTALLPETLGQPLPDTVQDLKSRSRGQNQQEQEQKQMMP	540
Qy	540	LQASAQEKNGL 550	
Db	541	LAOSTOEKNGL 551	

Qy 121 VTEWDLVCSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLILNYLQTAVSGTCAA 180  
 Db 115 VTEWNLVCSHRAFRQLAQSLFMVGVLLGAMMFGYLADRLGRRKVLILNYLQTAVSGTCAA 174  
 Qy 181 FAPNFPIYCAFRLLSGMALAGISLNCMTLNVEWMPHTRACVGTLLIGYVYSLGQFLLAGV 240  
 Db 175 YAPNYTVYCIFRLLSGMSLASIAINCMTLNMEWMPHTRAYVGTLLIGYVYSLGQFLLAGI 234  
 Qy 241 AYAVPHWRHLQLLVSAFFFAFFIYSWFFIESARWHSSSGRLDLTLRALQRVARINKREE 300  
 Db 235 AYAVPHWRHLQLAVSVFFFAFFIYSWFFIESARWYSSSGRLDLTLRALQRVARINKQEE 294  
 Qy 301 GAKLSMEVLRLASLQKELTMGKGQASAMELLRCPTLRHLFLCLSMWFATSFAYYGLVMDL 360  
 Db 295 GAKLSIEVLQTSLQKELTLNKGQASAMELLRCPTLRRLFLCLSMWFATSFAYYGLVMDL 354  
 Qy 361 QGFGVSIYLIQVIFGAVDLPKLVGFLVINSIGRRPAQMAALLLAGICILNNGVIPQDQS 420  
 Db 355 QGFGVSMYLIQVIFGAVDLPKLVGFLVINSIGRRPAQLASLLLAGICILVNGIIPRGHT 414  
 Qy 421 IVRTSLAVLGKGLAASFNCIFLYTGELYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE 480  
 Db 415 IIRTSIAVLGKGLAASFNCIFLYTGELYPTMIRQTGLGMGSTMARVGSIVSPLISMTAE 474  
 Qy 481 LYPSMPLFIYGAVPVAASAVTVLLPETLGQPLPDTVQDLESR-KGKQTRQQEHQKYMVP 539  
 Db 475 FYPSIPLFIYGAVPVAASAVTALLPETLGQPLPDTVQDLKSRSRGKQKQQLEQQKQMIP 534  
 Qy 540 LQASAEKKNGL 550  
 Db 535 LQVSTQEKKNGL 545

Sekine T et al., Expression cloning and characterization of a novel multispecific organic anion transporter. J Biol Chem. 1997 Jul 25;272(30):18526-9.